AMENDMENTS TO THE CLAIMS

Kindly cancel claims 78 and 79, amend claims 56, 74-77, 80, and 81, and add new claims 82-87 as provided in the following claims listing.

Claims Listing:

1.-55. (canceled)

56. (currently amended) The method of claim ~~79~~ 74, wherein the pre-sequence peptide is enzymatically cleaved from ~~the formed~~ said target peptide.

57.-73. (canceled)

74. (currently amended) A method of ~~using a selected pre-sequence to produce~~ synthesizing a target peptide ~~interest with~~ having the following structure:

$$X\text{-}AA_1\text{-}AA_2\text{.....}AA_n\text{-}Y,$$

wherein,

~~(1)~~ AA is an L or D amino acid residue,

~~(2)~~ X is hydrogen or an amino protective group,

~~(3)~~ Y is OH or NH_2, and

~~(4)~~ n is an integer greater than about 2 and less than about 60;

~~and further wherein the~~ said method ~~comprises the following steps~~ comprising:

a. coupling a pre-sequence peptide to a support, wherein said pre-sequence peptide comprises ~~selecting a pre-sequence comprising~~ from about 3 to about 9 amino acid residues having side chain functionalities which are, if necessary, protected during the synthesis, wherein each of the amino acid residues ~~are~~ has ~~independently selected from the group consisting of: L-amino acids and D-amino acids having~~ a propensity factor $P_\alpha > 0.57$ and a propensity factor $P_\beta \leq 1.10$, ~~and the corresponding D-amino acids,~~

b. ~~coupling the pre-sequence to a support as follows:~~

~~i. coupling an N-a-protected C-terminal amino acid selected from step (a),' to the support and subsequently removing the N-a-protecting group;~~

~~ii. coupling one or more amino acids selected from step (a) to the C-terminal amino acid from step b(i), wherein each coupling is performed in stepwise fashion and under conditions in which each amino acid is protected and subsequently de-protected, to form the pre-sequence;~~

~~iii.~~ coupling one or more N-α-protected amino acids to the N-terminus of the pre-sequence peptide or to a cleavable linker attached to the N-terminus of the pre-sequence peptide to form said target peptide ~~the peptide of interest~~, wherein each

coupling is performed in stepwise fashion and under conditions in which each of the amino acids of the target peptide is coupled and subsequently N-α-de-protected; wherein the pre-sequence peptide reduces or eliminates propensity of the target peptide ~~of interest~~ to adopt a β-sheet structure during the coupling and increases the coupling efficiency during the synthesis of the target peptide in comparison to the synthesis of the target peptide prepared under the same conditions without said pre-sequence peptide; and

c. cleaving ~~at least the peptide of interest~~ said target peptide from ~~the support~~ said pre-sequence peptide ~~to make the peptide~~.

75. (currently amended) The method of claims 74 or 82, wherein AA further comprises a side-chain protecting group.

76. (currently amended) The method of claims 74 or 82, wherein the pre-sequence peptide comprises amino acid residues that lack propensity to adopt the β-sheet structure.

77. (currently amended) The method of claim 74, wherein the method further comprises removing the N-α-protective group from the target peptide ~~of interest~~ before step (c).

78. (canceled) ~~The method of claim 74, wherein at step (c) the peptide of interest further comprises the pre-sequence~~.

79. (canceled) ~~The method of claim 78, wherein the method further comprises cleaving the pre-sequence from the peptide.~~

80. (currently amended) The method of claim 74, wherein the method further comprises at least one of the following steps: inserting a first linker between ~~peptide of interest~~ the target peptide and the pre-sequence peptide, and inserting a second linker between the pre-sequence peptide and the support.

81. (currently amended) The method of claim 80, wherein step (c) further comprises cleaving the first linker, the second linker or both the first and second linkers to produce the target peptide ~~of interest~~.

82. (new) A method of synthesizing a peptide conjugate having the following structure:

X-[target peptide]-[pre-sequence peptide]-Y,

wherein,

pre-sequence peptide is a homooligomeric peptide sequence consisting of from about 3 to about 9 amino acid residues having a propensity factor $P_\alpha > 0.57$ and a propensity factor $P_\beta \leq 1.10$,

target peptide is a peptide having the structure:

$$-AA_1-AA_2.....AA_n-,$$

AA is an L or D amino acid residue,

X is hydrogen or an amino protective group,

Y is OH or NH_2, and

n is an integer greater than about 2 and less than about 60;

said method comprising:

a. coupling a pre-sequence peptide to a support, wherein said pre-sequence peptide comprises amino acid residues having side chain functionalities which are, if necessary, protected during the synthesis,

b. coupling one or more N-α-protected amino acids to the N-terminus of the pre-sequence peptide to form said target peptide, wherein each coupling is performed in stepwise fashion and under conditions in which each of the amino acids of the target peptide is coupled and subsequently N-α-de-protected; wherein the pre-sequence peptide reduces or eliminates propensity of the peptide of interest to adopt a β-sheet structure

during the coupling and increases the coupling efficiency during the synthesis of the target peptide in comparison to the synthesis of the target peptide prepared under the same conditions without said pre-sequence peptide; and

c. cleaving said peptide conjugate from the support.

83. (new) The method of claim 82, wherein said pre-sequence peptide consists of from 5 to 7 amino acid residues.

84. (new) The method of claim 82, wherein said pre-sequence peptide consists of a polylysine.

85. (new) The method of claim 84, wherein said pre-sequence peptide consists of -$(Lys)_6$-.

86. (new) The method of claim 82, wherein the yield or purity of the peptide conjugate is increased in comparison to the synthesis of the target peptide prepared under the same conditions without said pre-sequence peptide.

87. (new) The method of claim 74, wherein the yield or purity of the target

peptide is increased in comparison to the synthesis of the target peptide prepared under the same conditions without said pre-sequence peptide.